

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 16:53:25 ; Search time 4492.43 Seconds
(without alignments)
6649.689 Million cell updates/sec

Title: US-09-830-647-3

Perfect score: 2780

Sequence: 1 aattgcgcgcgcgcgcctctctg.....aaaaaaaaaaaactcgcag 2780

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estom:*
5: em_estopl:*
6: em_estlba:*
7: em_estro:*
8: em_estov:*
9: em_hlc:*
10: qb_estl:*
11: qb_estl2:*
12: qb_hlc:*
13: qb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rtd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949.2	34.1	950	AL560180	AL560180 AL560180
2	817	29.4	845	AL581669	AL581669 AL581669
3	769	27.7	769	AL548911	AL548911 AL548911
4	768.2	27.6	784	AL573294	AL573294 AL573294
5	756	27.2	1019	AL573294	AL573294 AL573294
6	723.4	26.0	725	AL559244	AL559244 AL559244
7	721.6	26.0	903	AL559244	AL559244 AL559244
8	719	25.9	742	AL580899	AL580899 AL580899
9	713.4	25.7	2338	AL580899	AL580899 AL580899
10	712	25.6	712	AK014480	AK014480 Mus muscu
11	710.2	25.5	821	BF793466	BF793466 602254949
12	710	25.5	744	BG496289	BG496289 602538259
				AL948485	AL948485 wq060d08.x

13	692.4	24.9	703	11	BG716928	BG716928 602689445
14	691.6	24.9	767	11	BG717397	BG717397 602689720
15	671.4	24.2	701	10	AM960753	AM960753 EST372824
16	662.8	23.8	950	11	BE888697	BE888697 601513095
17	661.4	23.8	743	10	AI761101	AI761101 w16903.x
18	647	23.3	730	10	AM105287	AM105287 x459f02.x
19	645.4	23.2	659	10	BE613476	BE613476 601504243
20	639.4	23.0	927	11	BG025871	BG025871 602292007
21	627.4	22.6	629	11	BE888268	BE888268 601511791
22	597.8	21.5	603	10	AI824033	AI824033 w17909.x
23	593	21.3	616	11	BE884320	BE884320 601505790
24	586	21.1	701	10	BG722508	BG722508 602693762
25	585.8	21.1	610	10	AI805862	AI805862 t652d11.x
26	585	21.0	585	11	BG724408	BG724408 602689338
27	574.8	20.7	581	11	BG719249	BG719249 602690314
28	572	20.6	670	10	AV645569	AV645569 AV645569
29	568.2	20.4	706	11	BI094492	BI094492 602850523
30	561.6	20.2	839	10	BE564084	BE564084 601348046
31	561	20.2	561	10	AA451820	AA451820 z46f01.r
32	560.4	20.2	578	11	BG724066	BG724066 602697046
33	553	19.9	639	10	AV728361	AV728361 AV728361
34	548.6	19.7	935	11	EG341292	EG341292 602463961
35	548	19.7	549	10	AI923577	AI923577 w175c03.x
36	545.2	19.6	571	10	AU150504	AU150504 AU150504
37	540.2	19.4	760	11	BE219022	BE219022 601882245
38	523.8	18.8	839	10	BE782351	BE782351 601469844
39	517.8	18.6	533	10	AM631180	AM631180 h161905.x
40	493.4	17.7	570	10	AU143969	AU143969 AU143969
41	490.4	17.6	493	10	AI452459	AI452459 t162b12.x
42	488.6	17.6	626	10	BE245831	BE245831 TCBAPIE31
43	484.2	17.4	489	10	AM967974	AM967974 EST380049
44	479	17.2	668	11	BG168560	BG168560 602345241
45	478.4	17.2	740	11	BG965702	BG965702 602830553

ALIGNMENTS

RESULT 1
AL560180 950 bp mRNA
LOCUS AL560180 LTI_FL011_BCI Homo sapiens cDNA clone CSODG002YE20 5 prime
DEFINITION / mRNA sequence.
ACCESSION AL560180
VERSION AL560180.1 GI:12906394
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

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/clone="CSODG002YE20"
/clone_id="LTI_FL011_BCI"
/sex="male"
/tissue="B cells from Burkitt lymphoma"
/lab="host:DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen

Fri Dec 28 08:22:46 2001

us-09-830-647-3.rst

Page 2

BASE COUNT 303 a 204 c 209 g 232 t 2 others

[illegible]

Db 901 TTTTATCTTCAGCTGACCAATATGCCCTTTTATAAATTATTTCTATTCAGAR 950

RESULT	2
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LOCUS	AL581669 845 bp mRNA
DEFINITION	AL581669 lIT1.Ft011.Bc1 Homo sapiens cDNA clone CS0D6003YE20 3 prime
FEATURES	/ mRNA sequence.

SOURCE	Human
ORGANISM	<i>Homo sapiens</i>
REFERENCE	1 (bases 1 to 845)
AUTHORS	Li, W.B., Gruber, C., Joessee, J., and Poljasec, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope National de Sequencage

FEATURES	location/Qualifiers
source	1. .845

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSDBG002YE20"
/clone_1lb="Vt1_Ft011_Bc1"
/sex="male"
/tissue_type="R cells from Burkitt lymphoma"
/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with NotI and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
```

Query Match	29.48;	Score 817;	DB 10;	Length 845;
Best local Similarity	96.88;	Pred. No. 8.4e-123;		
Matches 818; Conservative	22;	Mismatches 4;	Indels 1;	Gaps 1

OY	1683	aatacaacagtgaagagagaatattcctttataaagagaccgaggaaactcgaaaaaagc	1742
Db	845	AATCAACAGTGAAGGAGCGAATAATTCTGTATTAAGACACCACAGAAACGAAAAAACGC	786
OY	1743	tccgtgttatttcgaagcccacgcccaaccttaaaagtattagggcgctaaatgga	1802
Db	786	TCCGTTATTATTTTAGGCCCATCCCCACCTTTCAAATGAATTSAGGGCCTTAATGAGA	726
OY	1803	aatgatgataaatagttcccttgtttaagtagcgctggaagatgcgacaataagacgaattta	1862
Db	725	AAATGAGATTAATTAATATTTTCATGTTTAAGTCAACGCTGAAGATGACATGAAGACAAATTTTA	666
OY	1863	cacagctaectacataataaaaacaaagaaatgattcttgacaattcggaaacaacat	1922
Db	666	CACAGCTACTCTTACTATTAATAAACAAACAGAAATGCATTTCTTGACATTTCCGAACACACAT	606
OY	1923	taagtgaanaatgacttaagaagactaaagggtagaatcatataaataatgatacatgagggt	1982
Db	605	TAAATGAAAATGACTTAGAGAGACCTAAAGGGTAAATATCTATCTATTAATGTMAATCACAGCAT	546
OY	1983	ctgtacatatgttcctg-atttcagtagcataatgatygalattccaaccaaaagaaafica	2041
Db	546	CTGTACATGTTTTTGCAATTCAGTACAGATAAATAGAGGATCTGCACAACAAACAGAAATCA	486

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QY 2042 gatactgctcttccagcaaaagatctcaagaaaagacccttcaatattact 2101
DB 485 GATACCTGCTTTTCCAGCAAAAGATCTCAAGAAAAGACCTTCATTCATATTACT 426
QY 2102 catgattctgctcgatatacaataaagcttcaagaagcaactctgcttcaagcaag 2161
DB 425 CATGATTCCTGCTGATATACATTAACGATTCACAAAGACACCTAACCTTCACGCCAAAG 366
QY 2162 gctccattccatccatccctccggaagaccacatgatatgcttcaagaataatgtagt 2221
DB 365 GCCCATTCCTMTCCCCCTCCCTSMSSMCCCAATGATGTSACTTCAAGATATGATAGT 306
QY 2222 ttacctctgttaaatacacacgaanaagtgaaataataatagagcgaataagaaagaa 2281
DB 305 TTMCBCTCTGCTRAATATCATCGAAAGAGRRRATATATTAGACGAATATGAAAGAA 246
QY 2282 aatctggaacaaatgctgtaatttgataaagaagactgaattattaccacaagaagaanaac 2341
DB 245 AATCTGGAACCAATGCTGAATTTGATTAAGAACTGAATTTATACAAAGAAAGAAAC 186
QY 2342 agaattttagtcccggtacagctcttactagacttgcttcaactagtgtaagaagaa 2401
DB 185 AGAATTTGTGCTTCCGCTACAGCTTACTAGACTTGTTCAGACTAGTGAAGAGAA 126
QY 2402 tcaagaattctgggtctcacaagctacacagaagaagagtgatagatgtttagat 2461
DB 125 TCAGATTTTGGGTTTACAGCTACACAGAAAGAGTGTATATGCAATGTTTAGAT 66
QY 2462 atttgggaaggaagaatcagataatctgttaacaagcgtttcttcgccccctcaact 2521
DB 65 ATTAGGAAGAGGAATTCAGATTAATCTGTAAACAGCGTTTCTCGTCCCHCAACT 6
QY 2522 tctac 2526
DB 5 TCTAC 1

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RESULT 3

AL548911 769 bp mRNA EST 16-FEB-2001

LOCUS AL548911 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1043Y010 5

DEFINITION prime, mRNA sequence.

ACCESSION AL548911

VERSION AL548911.1 GI:12884384

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 769)

AUTHORS L.I.W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVR cedex - France

Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.

FEATURES

source

1..769

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CS0D1043Y010"

/clone_lib="LTI_NFL006.PL2"

/library_type="Placenta"

/note="Vector: pCMVSPORT 6; Site: 1: NotI; 1st strand cDNA was primed with a NotI-Oligo(dt) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

Email : fliang@lifetech.com URL :

BASE COUNT 249 a 168 c 170 g 182 t

ORIGIN

Query Match 27.7%; Score 769; DB 10; Length 769;

Best Local Similarity 100.0%; Pred. No. 5e-115;

Matches 769; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 339 agccggtatccgccccgggaacccgactctgacagcggttactcttctggtagagcc 398

DB 1 AGCCGATCCGCGCCCGGAAACCCGACCTGACGCGGCTTACTCTGCTAGAGGC 60

QY 399 gtagcttgaggagaagagagcgccgctctctgtaacagcgccggggaagccgtctt 458

DB 61 GTAGCTGGCGGAGAGAGAGCGCGCGCTCTGTCAACAGCGCGGAGAGCGCTTCT 120

QY 459 cgggctcgccggtgagaaactctccgagcccaagcagtagtgccggcgactgcca 518

DB 121 CGCGCTGCGCGGTGGAGACCTTCTCCGACCCAGCATGTAGTGCGCGGACTGCCA 180

QY 519 tgaactcggagcaatgaagatccagagtaagagacattccaagggtggaatccaaagta 578

DB 181 TGAACCTCCGAGCCATGAGGATCCACAGTAAGACATTTCCAGGGTGGAAATCCAAGTCA 240

QY 579 aaaaagaaaacacagacatctctgaaatctctgaaatctgaaatctgaaatctgaaat 638

DB 241 AAAATGAAAAAAGACACCATCTGAAATCTGAAATCTGAAATCTGAAATCTGAAAT 300

QY 639 ccaattgtaagccacttggggaagaatcttactacttacttacttctgtaacatat 698

DB 301 CCAATGTAGCCACTTGGGAAAAAGTATTTACTTACTTACTTACTTACTTACTTACTT 360

QY 699 ctgaaanaactcaaaagacatgaagatctggaagcgagtggaagaattctcaga 758

DB 361 CTAAGAAACCTCAAAAGAGACATTAAGATCTGAGAGCGGAGCTGAAGATTTCTCAGCA 420

QY 759 aagatacagttatcttattcaataaagaagaagcctaatttgacacaaacttggtc 818

DB 421 AAGATATCATGTTATCTTATTTCAAAATGAAGAAAGTAAATTTGCAAACTTGGGTC 480

QY 819 gaattctcctgtacaaagtcgaatctgcaatactcagaacacattcaactcacc 878

DB 481 GAATTTCTCTGTACCAAGTCCAGATCTGCAATATCTGCAAGAAACCTTCACTCAGC 540

QY 879 ccagccatgaggaagttcaatttaagaccagacacagctgtgttgaagcagaagaaat 938

DB 541 CCAGCATGATGGAAGTTCAATTAAGTCAACAGACAGACAGTGTGTTAAAGCAAGAAAT 600

QY 939 tatgtgtgaaagacatacaagagacatgatttcttctccataatagatatataca 998

DB 601 TATTGATTAAAAAGCTATCAAGGACCATGATTTTATTTCTCAATATATATATTTCA 660

QY 999 atgccttgatcgggagagaaatctcatatgataagataactaactgaac 1058

DB 661 ATGCTTGTGATGGGAGAGTAAAAATTTCTCATATTTATATATATATATATATTTGAAC 720

QY 1059 aaaaagaaaagagtgtaatttactcaagaaatcaagtaactcaagtaag 1107

DB 721 AAAAGAAAAAGAGTGTATTTACTCAAGAAATCAAGTACTTCAAGTAAG 769

RESULT 4

AL573294 784 bp mRNA EST 16-FEB-2001

LOCUS AL573294 LTI_NFL006.PL2 Homo sapiens cDNA clone CS0D1043Y010 3

DEFINITION prime, mRNA sequence.

ACCESSION AL573294

VERSION AL573294.1 GI:12932397

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 784)
 AUTHORS Li, W. B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
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 /clone_lib="FRT_NFL006_PL2"
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9600 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifestech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 234 a 135 c 126 g 285 t 4 others
 ORIGIN

Query Match 27.6%; Score 768.2; DB 10; Length 784;
 Best Local Similarity 99.4%; Pred. No. 6.7e-115;
 Matches 778; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

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 DB 784 GGAATCATCTTTGACATTTCCGACACACATTAAGTGAATGACTTACAGACCTAAG 725
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OY 1951 ggttaagctcctaaatgaacacacagcagcagcagcagcagcagcagcagcag 2010
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 DB 724 GGTAAATCATCTTAATATGATATACATACAGCATCTGTACATGTTCTGATTCAGATACAGA 665
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OY 2011 taatatgagatctcaac 2069
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 DB 664 TAATAGTGAATCTCAAC 605
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OY 2070 tcaaggaagaagcctcattcaattactcaatgattcgtctgtgtaacaaataga 2129
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 DB 604 TCAAGGAAAAAGACCTTCATTCATTAATTAATTAATTAATTAATTAATTAATTAATTA 545
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OY 2130 gtccacaagaagcactaactgttcaaggcaaaagccatccatccatccctccgaagac 2189
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 DB 544 GTTCACAAGAGCACTTAACCTGTCAGCAAAAGCCYCCATTCATTCCTCTCTTAAGAAC 485
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OY 2190 ccaatgagctgagctcagaagaatagtatagtttactctctgttaaaatacagaag 2249
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 DB 484 CCAATGATGTGACTTCAAGATATAGTAGTTTACCTCTGTGTAATTAATTAATTAATTA 425
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OY 2250 tgaataataataatagaagaagaagaagaagaagaagaagaagaagaagaagaaga 2309
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 DB 424 TGAATAATAATTAAGACCAAAATGAAAAAATCTGGACCAAAATCTGGAATTTGATA 365
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OY 2310 aaagaactgaattatagaagaagaagaagaagaagaagaagaagaagaagaaga 2369
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 DB 364 AAAGACTGATTAATTAACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 305
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OY 2370 taactagcttgctcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2429
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 DB 304 TACTAGACTTGCTTTCAGACTAGTGAAGAGAAATACGAAATTTGGGTTTTCACAGACTTCA 245
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OY 2430 cagaaagaagctgtatataatgctttagatatttggagaagaagaagaagaagaaga 2489
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 DB 244 CAGAAAGAAGTGTATATGCAATGTTTATTTAGATATTTGGAGAGAGAGAGAGAGAGAGAG 185
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OY 2490 tgttaacagcagcttcttcctccctcaactctacattactgctcttaagaattaa 2549
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 DB 184 TGTTAACAGCGTTTTCCTCGCCCTTCAACTCTACATTAAGCTTTTGAATTTTA 125
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OY 2550 aaaaatcactcttcagaagtgatgaatcatctctgaatcttctaataatga 2609
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 DB 124 AAAATCATTAATTTTCAAGACTGATAGATATATCTTGAATTTTATTAATATGTA 65
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OY 2610 tggaaatctttagatcttcttaccagctctcttaccagaccacaaatgaatataaa 2669
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 DB 64 TGAATAATCTTGAATTTTATTTTACACACTTTGTTTACACGCCAAATTAATTTAAA 5
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OY 2670 ata 2672
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 DB 4 ATA 2

RESULT 5
 BG720949
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1019)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: gcrabs-remail.nih.gov
 Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shuraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 DNA distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM10737 row: 1 column: 03
 High quality sequence stop: 785.
 Location/Qualifiers
 1..1019
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 /db_xref="taxon:9606"
 /clone_lib="NIH-MGC_97"
 /clone_lib="NIH-MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pluescript (modified
 pluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (9cgaag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTT-3',
 size selected for average insert size 2.2 kb and
 normalized to 10^5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH-MGC library."

BASE COUNT 320 a 221 c 248 g 230 t
 ORIGIN

Query Match 27.2%; Score 756; DB 11; Length 1019;
 Best Local Similarity 94.6%; Pred. No. 6e-113;
 Matches 838; Conservative 0; Mismatches 40; Indels 8; Gaps 5;

OY 337 ggaagcagatccgccccggaagccagcagcagcagcagcagcagcagcagcagcag 396
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 DB 5 GAGAGCGATCGCGCGCGGAGAAACCGACCTGACAGCCGCTACTCTACTGCTAGAGG 64
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QY 397 cggatctgcggaaggaagagcgccgtctctgcaacagccggggaagcgtgct 456
DB 65 cggatctgcggaaggaagagcgccgtctctgcaacagccggggaagcgtgct 124
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DB 125 ttccggcgcccgccggcgagcacccttctccggaccagcgtgaagtgccggcgagctgc 184
QY 517 catgaactccggagccatgaagatccacagtaaaagacattccagggtggaatccaagt 576
DB 185 catgaactccggagccatgaagatccacagtaaaagacattccagggtggaatccaagt 243
QY 577 caaaatgtaaaaaaagaagacatctctgaaatctctgaaactgtaaaagccagaaaaa 636
DB 244 caaaatgtaaaaaaagaagacatctctgaaatctctgaaactgtaaaagccagaaaaa 303
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DB 304 atccaaatgtaaaagcacttggggaaaagatatttaccctgtaactcctctgcaaat 363
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DB 364 atctgaaaaactccaagaagacatlaagagatctgggaagcgagctggaagaattctcag 423
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DB 424 caaagatcatgattatctatttcaaat--gaaggaagcctaatttgcacaacctg 483
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DB 544 catcccaagcatalgaggaagttcaatlaagtcacagacagtgctgtaagcagaaga 603
QY 935 aaattttagtggaaaagcatalcaagaagcatttatttccctccaatattatatta 994
DB 604 aaattttagtggaaaagcatalcaagaagcatttatttccctccaatattatatta 663
QY 995 tcaaatgacctgtcagggggaagtaaaatctctcatatgata--ttagatattcat 1053
DB 664 tcaaatgacctgtcagggggaagtaaaatctctcatatgata--ttagatattcat 723
QY 1054 tgaacaaaagaagaagtgctgatttactcaagaagaatccaagtaac--ttcagtaagagatg 1112
DB 724 tgaacaaaagaagaagtgctgatttactcaagaagaatccaagtaac--ttcagtaagagatg 783
QY 1113 ggggcaaaaagagtgctgattgctgcaaaaaaacaagaagaagcctaanaagcctt 1172
DB 784 ggggcaaaaagagtgctgattgctgcaaaaaaacaagaagaagcctaanaagcctt 843
QY 1173 ttgtaaggtggaagatagcacaacttatagggcatttactt 1218
DB 844 gggttagcgtgagatgagc--ccactttatagccctttttagctt 886

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RESULT 6
AL559244 725 bp mRNA EST 16-FEB-2001
LOCUS AL559244.L1_NFL008.TC2 Homo sapiens cDNA clone CSDDJ012YI06.5
DEFINITION prime, mRNA sequence.
ACCESSION AL559244
VERSION AL559244.1 GI:12904555
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 725)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization

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JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: segreif@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
source
1..725
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSDDJ012YI06"
/location="L1_NFL008.TC2"
/sex="male"
/tissue.type="T cells from T cell leukemia"
/notes="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 224 a 166 c 164 g 171 t
ORIGIN
Query Match 26.0%; Score 723.4; DB 10; Length 725;
Best Local Similarity 99.9%; Pred. No. 1.2e-107;
Matches 724; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 329 cggcgcttgagccggatccggcccggaacccgacctcagaagcgggtaactctg 388
DB 1 cggcgcttgagccggatccggcccggaacccgacctcagaagcgggtaactctg 60
QY 389 cgtagaagccgtagctggcggaaggaagagggcgctctctgcaacagccggggaa 448
DB 61 cgtagaagccgtagctggcggaaggaagagggcgctctctgcaacagccggggaa 120
QY 449 gccgtgcttcggcgctccggcgtgcaacattctccggaccagatgtaagtgccg 508
DB 121 gccgtgcttcggcgctccggcgtgcaacattctccggaccagatgtaagtgccg 180
QY 509 ggcagctgcaatgaactccggagccatgaagatcacaagtaaggaattccaggtgga 568
DB 181 ggcagctgcaatgaactccggagccatgaagatcacaagtaaggaattccaggtgga 240
QY 569 atccaagtcataaaatgaataaacaagacatctctgaatctctgaagaactgaacag 628
DB 241 atccaagtcataaaatgaataaacaagacatctctgaatctctgaagaactgaacag 300
QY 629 ccagaataatccaaatgtaagcacttggggaagatatttacccttgacttaccctt 688
DB 301 ccagaataatccaaatgtaagcacttggggaagatatttacccttgacttaccctt 360
QY 689 gtaacatattctgaataactcacaagaacatgaagatctggagggcgagtggaaga 748
DB 361 gtaacatattctgaataactcacaagaacatgaagatctggagggcgagtggaaga 420
QY 749 ttctcagaagaatcatcattatctatttcaataaagaagaagcctaattgcaaa 808
DB 421 ttctcagaagaatcatcattatctatttcaataaagaagaagcctaattgcaaa 480
QY 809 acctgggtcgaaatttctctgtacccaagtcagaatctgatactatgcagaacact 868
DB 481 acctgggtcgaaatttctctgtacccaagtcagaatctgatactatgcagaacact 540
QY 869 tcaactatcccgagcatgtaggaagttcaatttaagtcaccagacagatggttttaagc 928
DB 541 tcaactatcccgagcatgtaggaagttcaatttaagtcaccagacagatggttttaagc 600
QY 929 aagaagaattatagttgaaaagcattcaagaagcatttatttacccttcaaatag 988

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Db 601 AGAGCAAAATTATTAGTTGAAAAAGCTATCAAGACATGATTTTATTCCTTCAAAATAGT 660
OY 989 atactataaactccttcacagaggagtaaaatcttccatattgagacattgagac 1048
Db 661 AATATATCAAAATGCTTGATCGGAGATAAATAATCTTCAATTTCATGACATAGATAC 720
OY 1049 tacat 1053
Db 721 TACAT 725

RESULT 7
LOCUS AU128881 903 bp mRNA EST 24-OCT-2000
DEFINITION AU128881 NT2RP2 Homo sapiens cDNA clone NT2RP2004396 5', mRNA
sequence.
ACCESSION AU128881
VERSION AU128881.1 GI:10989235
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 903)
AUTHORS Ota,T., Nishikawa,Y., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isoqal,T.
HRI human cDNA project
Unpublished (2000)
JOURNAL Contact: Takao Isoqal
COMMENT Genomics Laboratory
Helix Research Institute
153-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project: 5' & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute
FEATURES
source
1. 903
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RP2004396"
/cell_line="NT2RP2"
/cell_type="Leukocarcinoma"
/clone="Vector: PME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction."
BASE COUNT 326 a 165 c 157 g 242 t 13 others
ORIGIN
Query Match 26.0%; Score 721.6; DB 10; Length 903;
Best Local Similarity 92.3%; Pred. No. 2.3e-107;
Matches 820; Conservative 0; Mismatches 56; Indels 12; Gaps 6;

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OY 1893 aatgactcttgacattccgaaacacacattgaagaatgactagaagaactaagg 1952
Db 241 AATGATTTCTTGACATTTCCGACACATTAAAGTGAATAATGCTTAAGAACTAGG 300
OY 1953 tagatcacataaagtgacatacagaacatcgtacatgcttctcgtatcagtagacata 2012
Db 301 TAGATCATAATAAGTAAACATACAGCATCTGACATGCTTCTGATTTAGTACAGATA 360
OY 2013 atagatgacttaacaaacaaagaagatcagatcgtctcttccacagaagatcca 2072
Db 361 ATAGTATCTACACCAAAAGCAAGATCACTAGTCTGCTTTCCAGCAAAAGATCTCA 420
OY 2073 agaaaagagacttcaataatctcgtatgctcgtctgctgtaacaaataaagtt 2132
Db 421 AGCAAAAGACCTTCATTCATATTTACTCATGATCTGCTGATTAACATTAACAGTT 480
OY 2133 cacaagagcactaactgttcaggaagagctccatctcctcctcgaagacc 2192
Db 481 CACAAGAGCACTTACCTGTTCCAGCNAAGGCTCCATTCATCTCTCTGAGACCA 540
OY 2193 atgaatgactcaagaatacgaatgattacacttcgtgtaaaatacgcgaagtg 2252
Db 541 ATGAATGTGACTTCAAGATATGATGATTTACCTCTGTGTAATAATCAATCAAAAGTCA 600
OY 2253 aataatatta-gaacgaatagaaagaagaatcgtgaacaaatcgtgaattgataaa 2311
Db 601 AATATATTTAGGAGCAAGATATGAAATCAAAATCTGAAACCAATGCTGATTTGATAAA 660
OY 2312 agaactaatatttatacagaagaagaagaatctgtatgctacacgtacagcttta 2371
Db 661 AATATATTTATTTTCCCAACAGAAACAAACGATTTGT-TTCCACGGGTACAGCTTTA 719
OY 2372 ctgaactgtttcagactagtaagaagaagaatctgtatgctacacgtacagcttta 2431
Db 720 CTAAACGTTTTCAGACTAGTGAATAAATCAATCAATTTTGGCTTTCCAAACGCTACCA 779
OY 2432 gaaaa--gagtgatataagcaatgctttagatattgg-----aagagaagaatcga 2484
Db 780 GAAAAAGAAATTGATATATCCCATGTTTAAATATTTGGGAAAAAAGAAATTTCCANAT 839
OY 2485 taatcgttaacagcgctttt--ctcgtcccttaacttcaacttcaactt 2530
Db 840 AATCTGTTTACAGCGTTTTCCTCCCGTCCCTCCACTTCTTCMT 887

RESULT 8
LOCUS AL580899 742 bp mRNA EST 16-FEB-2001
DEFINITION AL580899 LTI_NFL008_TC2 Homo sapiens cDNA clone CS0D012YL06 3
prime, mRNA sequence.
ACCESSION AL580899
VERSION AL580899.1 GI:12947367
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 742)
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Poyles,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr.
FEATURES
source
1. 742
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D012YL06"
/cell_line="LTI_NFL008_TC2"
/sex="male"

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primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.

Note: this is a NIH_MGC library.

BASE COUNT 275 a 122 c 135 g 180 t
ORIGIN

Query Match 25.6%; Score 712; DB 11; Length 712;
Best Local Similarity 100.0%; Pred. No. 8.4e-106; Mismatches 0; Indels 0; Gaps 0;

Matches 712; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1233 tgccttataataattatctatctcagaagccctgcagctcattatgtatgagaagccat 1292
1 tgccttataataattatctatctcagaagccctgcagctcattatgtatgagaagccat 60
1233 ctatgatacaaaagcaaacctcaggttaaaactaagaatccaacagatgagatg 1352
61 ctatgatacaaaagcaaacctcaggttaaaactaagaatccaacagatgagatg 120
1353 gtggaacctcaatcaactccaggttgaaagagaagaaaaagatatgtgaatgt 1412
121 gtggaacctcaatcaactccaggttgaaagagaagaaaaagatatgtgaatgt 180
1413 gcttcagaagaatgaaagatcagaactcaccctcctaagtgagagaacagaacttg 1472
181 gcttcagaagaatgaaagatcagaactcaccctcctaagtgagagaacagaacttg 240
1473 caagagaagaacagatcagaactcaggttgatgatcattgtatcagtttlltgaacttg 1532
241 caagagaagaacagatcagaactcaggttgatgatcattgtatcagtttlltgaacttg 300
1533 tgggaatgaaagagac 1592
301 tgggaatgaaagagac 360
1593 ctccctgttctcgaagtgctcctgaaagaaagactgaaacaaagaaagtgatgcaac 1652
361 ctccctgttctcgaagtgctcctgaaagaaagactgaaacaaagaaagtgatgcaac 420
1653 alattctcagaagaactgcgaagagatgatacaacagtgagagagcaaatcttcgt 1712
421 atatttttcagaaagattgcccagaaagatgatacaacagtgagagagcaaatcttcgt 480
1713 ataagagaacacaggaactgaaagaaagctcctgttattctcagaagccatccccac 1772
481 ataagagaacacaggaactgaaagaaagctcctgttattctcagaagccatccccac 540
1773 ctccaatgaactgagagagcttaatgagaaatgataataatcttcagtgtaagta 1832
541 ctccaatgaactgagagagcttaatgagaaatgataataatcttcagtgtaagta 600
1833 cagctgaagatgatacagaacagaaatttacacagctacactacataaataaacaacag 1892
601 cagctgaagatgatacagaacagaaatttacacagctacactacataaataaacaacag 660
1893 aatgactcttgacatcttcgagacaacatlaagtgaagaatgacttagaga 1944
661 aatgactcttgacatcttcgagacaacatlaagtgaagaatgacttagaga 712

RESULT 11
BG496289 821 bp mRNA EST 27-MAR-2001
LOCUS 602538259P1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4659446 5',
DEFINITION MRA sequence.
ACCESSION BG496289
VERSION BG496289.1 GI:13457805
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 821)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
CONTACT: Robert Strausberg, Ph.D.
COMMENT Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://Image.llnl.gov>
Plate: L10C1455 row: e column: 15
High quality sequence stop: 742.

FEATURES

source

1. 821
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4659446"
/clone_lib="NIH_MGC_59"
/tissue_type="mucoepidermoid carcinoma"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: Lung; Vector: pDNR-LIB (Clontech); Site: 1:
SfiI (ggccgctcgcc); Site 2: SfiI (ggccatattgccc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATCTAGAGCGGAGGGCGGACATG-dT(30)BN-3-
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
library."

BASE COUNT 273 a 166 c 176 g 206 t
ORIGIN

Query Match 25.5%; Score 710.2; DB 11; Length 821;
Best Local Similarity 96.8%; Pred. No. 1.6e-105;
Matches 799; Conservative 0; Mismatches 18; Indels 8; Gaps 7;

417 gaggcgccgctcctctcgaagagccgagggagccgtgcttcggagctgcgcgtgga 476
1 gaggcgccgctcctctcgaagagccgagggagccgtgcttcggagctgcgcgtgga 60
477 cacttctcggagccagatgtaagtgccggcgagctgcagtaactccggagcatga 536
61 cacttctcggagccagatgtaagtgccggcgagctgcagtaactccggagcatga 120
537 ggaaccagaaagacattccagggtggaatccaagtcacaaatgaaaaaacacagc 596
121 ggaaccagaaagacattccagggtggaatccaagtcacaaatgaaaaaacacagc 180
597 catctctgaaatctctgaaactgataacagcgccgagaaaaatccaatgtaagccactt 656
181 catctctgaaatctctgaaactgataacagcgccgagaaaaatccaatgtaagccactt 240
657 ggggaaagatatttacccttgactcctctcgtgcacatctatctgaaaaactcaaaag 716
241 ggggaaagatatttacccttgactcctctcgtgcacatctatctgaaaaactcaaaag 300
717 acattaaagatctggagagcgagtgaaagaatttccagcaagaatcagttactta 776
301 acattaaagatctggagagcgagtgaaagaatttccagcaagaatcagttactta 360
777 ttccaataagaagagactaaatttgacacaaaccttggtgtaatttctctgtaccaa 836
361 ttccaataagaagagactaaatttgacacaaaccttggtgtaatttctctgtaccaa 420
837 gcccaagaatctgaatctatgagaacacactcactcactatcccaacagatgagaagt 896
421 gtccagaatctgaatctatgagaacacactcactcactatcccaacagatgagaagt 480

QY	897	catlaagatcacagagacacatgctgtttaagcagcagggagaaattcttgatgtgaaaaagccta	956
Db	481	catTTTAAGTGCACAGACACAGCTGTGTTTAAGCAGAGGAAATTTATGAGTGGAAAAAGCTA	540
QY	957	tcaagcgcattgatttatttccttccaattgtcatalatctcaaaagcc-tgtcatagggga	1015
Db	541	TCAGAGCAACATGATTTTATCTCTTCAAAATGATATTTATCAATACCTCTTGTCATGGGA	600
QY	1016	gtcaaaattcttcataatgaiga-catlagatactacatlgacacaaaagaagaagctt	1074
Db	601	GTAAAAATTTCTTATATTCATGACCTTTACATATCATTTGATGAC-AGAGTGGTGGC	659
QY	1075	gtattactcctcaagaatcctagcttacttcagtaagaagatggggcgaagaagttgtagtg	1134
Db	660	GTAATTACTCAGAAATATCATGACTCATGATAGAGATGGGGGCAAA--GAGTGGTGGC	717
QY	1135	tgcacaaaaaacagagacagcaggaagaccctcaaaaagccttttgtaaggttggaagatctgag	1194
Db	718	TCGACAAAAAACAAGAACAGAGAACTCAAAAGCCTTTTGGT-AAGGTGGCAGATATGAG	776
QY	1195	ccactctatagcgcatttacttcttcagctgcagcaatatgccttt	1239
Db	777	CCAA-TTTATAGGCCA-TTTATCTTCAAGCTGACAGATATGACCTTT	819
RESULT	12		
A1948485/C			
LOCUS	A1948485	744 bp	mRNA
DEFINITION	wg66d08.x1 NCI-CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470479 3' similar to: R:075226 075226 WUSC:R:RG135C18.1 PROTEIN ;, mRNA sequence.		
ACCESSION	A1948485		
VERSION	A1948485.1	GI:5740795	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.		
REFERENCE	1 (bases 1 to 744)		
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .		
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index		
JOURNAL	Unpublished (1997)		
COMMENT	Contact: Robert Strussberg, Ph.D. Email: cgap@nci.nih.gov Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html Insert Length: 1484 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 432. Location/Qualifiers 1. 744 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:2470479" /clone_lib="NCI-CGAP_Kid12" /tissue_type="2 pooled tumors (clear cell type)" /lab_host="DH10B" /note="Organ: Kidney; Vector: pTT3D-pac (Pharmacia) with a modified polylinker; Site:1; Not 1; Site:2; Eco RI; Plasmid DNA from the normalized library NCI-CGAP_Kid5 was prepared and ss circles were made in vitro. Following BamHI purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1323912-1325831, 1471368-1472903 and		

BASE COUNT	223 a	127 c	117 g	277 t	
ORIGIN	1492104-1493255) " Subtraction by Bento Soares and M. Fatima Bonaldo. "				
Query Match	25.5%; Score 710; DB 10; Length 744;				
Best Local Similarity	97.3%; Pred. No. 1.8e-105;				
Matches 722:	Conservative	0;	Mismatches	20;	Indels 0; Gaps 0;
Db	1961	tataaatatacctaacgagcatctgtacattcttcttattctggtacacataataatgtaga	2020		
Db	744	TATCAATGTATACAAACAGGCGTCGTACACTGTTCTGATCTCGATCAATCAATGATGGA	685		
Qy	2021	tctcaacacaaacgaagatgaagactgtgtcttcttcagcaagaagatctcaagaag	2080		
Db	684	TCTCAACGACGACCAAGTCAAGTACTGTGCTTTTTCACCAAGATCTCAAGGAACAG	625		
Qy	2081	gacctcattcaataattactatctgaattctgtgtgtataacaaataaagttccagaag	2140		
Db	624	GACCTTCATTCGATATTTACTCTCATGATGTGTGCTGTGATACATTAACAGTTCCACAG	565		
Qy	2141	caacttaactgtctcagcaagagctccatctcaatctcaatctctccctcaggaacccaatgagt	2200		
Db	564	CACCTTAACGCTTCACGCAAGGCTCCATTCCTCATCTCTGTATGAGAACCCATGAAATG	505		
Qy	2201	gacttcaagaatagtagaatagtttaccctctgtgtataaataacacgaagaagtgaaataata	2260		
Db	504	GACTTCATTAAGATATGATAGTACTTTTACCTTGTGTAAATACATGCAAAAGTGAAATTAATA	445		
Qy	2261	cttgagacggaataagaaagaataatctcgagaccaaatgctgaattctgataaagaactgaa	2320		
Db	444	TTAGGACGCAAAATGCAAAAGAAATCTGCAACCAATGCTGAATTTGATTAAGAACTGA	385		
Qy	2321	tctattcaacaagaagaacaaagaatttgtagttcacccgtgtacagttcttactgacttg	2380		
Db	384	TTTATTACACAGAGAAACAAACAAATTTGTATGTTACCGGATACAGCTTTTACTATACATTG	325		
Qy	2381	tttcacagactagtagaagaagaatacagaattcttggtgttcacaaagctacacacagaagaagt	2440		
Db	324	TTTCAGACATAGTGAAGACAAATCTGAAATTTTGGGTTTCACAAAGCTAACACAAAAAGAGT	265		
Qy	2441	ggtatactgaagaatttagatatttggaagtagaagaagaatactcagataactgtttaaaccg	2500		
Db	264	GGATATATGCATGTTTATGATATTTGGAAAGGAAATTCAGATATCTGTTAAACACCG	205		
Qy	2501	ttttctctgtcccttcaactctcaacttcaacttcaactgagcttctgaatttaaaaaatgcacac	2560		
Db	204	TTTTTCGCTGCCCTTCAACTCTTCAACTTACAGCTTTTGATATTTAAAAATTCATATC	145		
Qy	2561	ttttcgaagatagtaagaataatacttcttgaatttttaataatagtagagaactctc	2620		
Db	144	TTTTCAAAATGATTAAGATATATTTCTTGAATTTTATTAATATATGAAATTCCT	85		
Qy	2621	aggaatttttttaccagcttctttaaagaccaaatgtaaatatataaaataaataatcttg	2680		
Db	84	AGGATTTTTTTTACCGACTTGTATTACAGACCCCAATGTAAATATTAAAAATTAATTTTG	25		
Qy	2681	caatttctcagagaattcgataa	2702		
Db	24	AAAAAATCTAAAAA	3		
RESULT 13					
LOCUS	BG716928	703 bp	mRNA	EST	08-MAY-2001
DEFINITION	602869445F1 NR_HMG_97 Homo sapiens CDNA clone IMAGE:4821970 5', mRNA sequence.				
ACCESSION	BG716928				
VERSION	BG716928.1	GI:13996115			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				

LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
293	gcagccactgcttcttgcttgcctctctcctcgcgccttgagacgcgalcgcgc	352								
62	GCAGCCACTCTTTTGCTGTGCTTTGGCCCTTCCTCTCCGGCCCTGGAGCCGATCCGGCC	121								
353	ccggaacaccgcagccctgcagacgcgcgttaacctactctactcgtctagagccgccttagctgcgcgcgc	412								
122	CCGGAACCCCGACCTCGACGAGCGCGGTACCTCTCTCCGCTAGAGCGCGTACGTGGCGGAAG	181								
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AW960753	AUTHORS	Hedge, P., Ol, R., Abernathy, K., Dharap, S., Gaspar, R., Gay, C., Holtz, J., Saeed, A. I., Sharov, V., Lee, N. H., Yeaman, T. J. and Quackenbush, J.								
AW960753	TITLE	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray								
AW960753	JOURNAL	Unpublished (2000)								
AW960753	COMMENT	Contact: John Quackenbush The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528 Fax: 301 838 0208								

Email: johng@tigr.org									
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